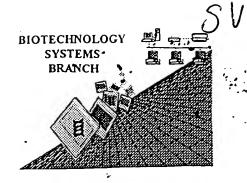
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09786635

Source: 11/1401

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/786635
ATTN: NEW RULES CAS	ES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P
1Wrapped Nucleics Wrapped Aminos	The numberhest at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
JMisaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use apace characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
SVariable Length.	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in Patentin version 2.0 has equited the <220> <223> section to be missing from a mino acid sequences(s) Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220> <223> section to the subsequent amino acid sequence. This applies to the mandatory <220> <223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
<i></i>	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to Include the skipped sequences.
Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence(210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
0Invalid <213> Response	Per 1.823 of Sequence Rules, the only valld <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus) species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence
Usc of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
Patentin 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
Misuse of n	in can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

PCT09

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RAW SEQUENCE LISTING DATE: 11/14/2001 PATENT APPLICATION: US/09/786,635 TIME: 14:04:22
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Output Set: N:\CRF3\11142001\I786635.raw

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Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\1786635.raw

236 237	Gln	Ala	Ile 435	Arg	Thr	Ile	Ser	Arg 440	Phe	Met	Glu	Cys	Val 445	Asn	Leu	Asn
	Lys	Leu		Pro	Ile	Ala	Thr		Val	Trp	Leu	Ile		Lys	Ser	Met
240		450					455					460				
242	Glu	Leu	Leu	Asp	Glu	Arg	Lys	Phe	Trp	Ala	Gly	Ile	Val	Phe	Thr	Gly
	465			_		470	_		_		475					480
245	Ile	Thr	Pro	Gly	Ser	Ile	Glu	Leu	Pro	His	His	Val	Lys	Tyr	Lys	Ile
246				-	485					490			_		495	
248	Arg	Met	Asp	Ile	Asp	Asn	Val	Glu	Arg	Thr	Asn	Lys	Ile	Lys	Asp	Gly
249	-		_	500	_				505					510		
251	Tyr	Trp	Asp	Pro	Gly	Pro	Arg	Ala	Asp	Pro	Phe	Glu	Asp	Met	Arg	Tyr
252			515					520					525			
254	Val	Trp	Gly	Gly	Phe	Ala	Tyr	Leu	Gln	Asp	Val	Val	Glu	Gln	Ala	Ile
255		530					535					540				
257	Ile	Arg	Val	Leu	Thr	Gly	Thr	Glu	Lys	Lys	Thr	Gly	Val	Tyr	Met	Gln
258	545					550					555					560
260	Gln	Met	Pro	Tyr	${\tt Pro}$	Cys	${\tt Tyr}$	Val	Asp	Asp	Ile	Phe	Leu	Arg	Val	Met
261					565					570					575	
263	Ser	Arg	Ser	Met	Pro	Leu	Phe	Met	Thr	Leu	Ala	Trp	Ile	Tyr	Ser	Val
264				580					585					590		
266	Ala	Val		Ile	Lys	Gly	Ile		Tyr	Glu	Lys	Glu		Arg	Leu	Lys
267			595					600					605			
269	Glu	Thr	Met	Arg	Ile	Met	_	Leu	Asp	Asn	Ser		Leu	Trp	Phe	Ser
270		610					615					620				
	_	Phe	Ile	Ser	Ser	Leu	Ile	Pro	Leu	Leu		Ser	Ala	Gly	Leu	
	625					630	_ =	_	_	_	635	_	_	_	_	640
	Val	Val	Ile	Leu		Leu	GTA	Asn	Leu		Pro	Tyr	Ser	Asp		Ser
276				1	645		~	1	51 -	650	** 1	**- 1	ml	-1.	655	Q1
	vaı	vaı	Pne		Pne	Leu	ser	vaı		Ala	vaı	vaı	Thr		Leu	GIN
279	0	nh -	T	660	C	mb	т о	nha	665	7 ~~	7 1 a	7 an	T 011	670	3] -	31 5
	Cys		675	тте	ser	Thr	ьeu	680	ser	Arg	Ата	ASII	685	Ата	Ата	нта
282	0	C1		т1.	Tla	Tyr	Dho		T 011	marx.	T OU	Dro		Wa I	T 011	Cvc
285	Cys	690	СТА	TTE	тте	TAT	695	1111	Leu	тут	ьеи	700	TAT	val	ьеu	Cys
	Val		Фrn	Cln	λcn	Tyr		C1v	Dho	Thr	Len		Tla	Dho	λla	Sar
	705	нта	тъ	GIII	АЗР	710	vai	GTĀ	PHE	1111	715	пуэ	116	FIIC	Ala	720
		Lau	Sor	Dro	V a l	Ala	Dhe	G1 ₃₇	Dha	Glv		Glu	Туг	Dho	Δla	
291	Deu	цец	DET	FIO	725	AIG	rne	Gry	riie	730	Cys	Olu	1 Y 1	THE	735	DCu
	Dho	Glu	Glu	Gln		Ile	Glv	Val	Gln		Δsn	Δsn	T.011	Dhe		Ser
294	1 110	GIU	GIU	740	GLY	110	O L y	VUI	745	115	пор	11511	LCu	750	Olu	UCI
	Pro	Va 1	Glu		Asn	Gly	Phe	Asn		Thr	Thr	Ser	Va l		Met	Met
297	110	, u _	755	Olu	1156	017	1	760	J.Cu			001	765	001		
	Leu	Phe		Thr	Phe	Leu	Tvr		Val	Met	Thr	Trp		Ile	Glu	Ala
300		770					775	1				780	- <u>,</u> -			
	Val		Pro	Glv	Gln	Tyr		Ile	Pro	Arq	Pro		Tyr	Phe	Pro	Cys
	785			-1		790	- 4				795	~	•			800
		Lys	Ser	Tyr	Trp	Phe	Gly	Glu	Glu	Ser		Glu	Lys	Ser	His	
306		-		-	805		-			810	-		-		815	
	Gly	Ser	Asn	Gln	Lys	Arg	Ile	Ser	Glu	Ile	Cys	Met	Glu	Glu	Glu	Pro
	_				_	-										

09/186635

Page & 50f8B

```
<210> 3
<211> 1130
<212> DNA
<213> Human
<220>
<223> human cDNA of ABCB9
```

```
<400> 3
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agggcgccca gctgtcaggt ggccagaagc agcgggtggc catggccgng gctctggtgc 120
ggaacccccc agtcctcatc ctggatgaag ccaccagcgc tttggatgcc gagagcgagt 180
atctgateca geaggeeate catggeaace tgteagaage acaeggtaet cateategeg 240
caccadeta describina describina esta esta esta de la compacta del compacta de la compacta de la compacta del compacta de la compacta del la compacta de la compacta del la compacta de la 
gtgcagcagg gcacccacca gcagcttgct tgccccaggg cgggctttta cggcaagqt 360
gttqcaqcqq caqatqtqqq gtttcaaggc cgcagacttc acagctggcc acaacgagcc 420
tgtagccaac gggtcacaag gcctgatggg gggcccctcc ttcgcccggt ggcagaggac 480
ccggtgcctg cctggcagat gtgcccacgg aggtttccag ctgccctacc gagcccaggc 540
ctgcagcact gaaagacgac ctgccatgtc ccatgatcac cgcttnbgca atcttgcccc 600
tggtccctgc cccattccca gggcactctt acccennnct gggggatgtc caagagcata 660
gtcctctccc catacccctc cagagaaggg gcttccctgt ccggagggag acacggggaa 720
cgggattttc cgtctctccc tcttgccagc tctgtgagtc tggccagggc gggtagggag 780
cgtggagggc atctgtctgc caattgcccg ctgccaatct aagccagtct cactgtgacc 840
acacgaaacc tcaactgggg gagtgaggag ctggccaggt ctggaggggc ctcaggtgcc 900
cccagcccgg cacccagett tegececteg teaatcaace cetggetgge ageegeeete 960
cccacacccg cccctgtgctctgtctg gaggccacgt ggaccttcat gagatgcatt 1020
ctcttctgtc tttggt gan grgatggtgc aaagcccagg atctggcttt gccagaggtt 1080 gcaacatgtt gagagaaccc ggtcaataaa gtgtactacc tcttacccct 1130
```

Untersorm must be enumerated on fields 221, 222 and 223

Glokan

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY DATE: 11/14/2001 PATENT APPLICATION: US/09/786,635 TIME: 14:04:23

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\1786635.raw

```
L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:579 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:579 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:580 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:580 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:584 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:584\ M:258\ W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:588 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:588\ M:258\ W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:589 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L 589 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:596 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L 写96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L 23 M: 258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L \stackrel{\text{\tiny $623}}{=} 23 \text{ M}:258 \text{ W}: Mandatory Feature missing, <222> not found for SEQ ID#:4
L 623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:624 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:624 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L 205 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L 205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:$\frac{1}{205} M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L 1212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L \square212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L=212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1213 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1213\ M:258\ W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1214 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:1214 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:1214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1577 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:1577 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1625 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:1625\ M:258\ W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:1625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1720 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1720 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1986 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/786,635

DATE: 11/14/2001
TIME: 14:04:23

Input Set : A:\Lea33298.app

Output Set: N:\CRF3\11142001\I786635.raw

```
L:1986 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1988\ M:258\ W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1988 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1988 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1990 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1990\ M:258\ W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1990 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1993 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1993 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1994 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1994 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1995 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1995 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L資995 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L 變013 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:2013 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L$\overline{\pi}$013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L2014 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L型014 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L_{2}014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L_{12}^{12}289 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L:2289 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L 2289 M: 341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L 2291 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:54
L^{1/2}291 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:54
L 2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 L 2293 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L_{2296} M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
```